What is claimed is:

1. An oligonucleotide primer selected from the group consisting of SEQ ID NOs: 10-30.

2. A pair of oligonucleotide primers, wherein said pair consists of at least one primer of claim 1.

3. A pair of oligonucleotide primers, selected from the group consisting of:

a) SEQ ID NO: 30 and SEQ ID NO:4;

b) SEQ ID NO:27 and SEQ ID NO:4;

c) SEQ ID NO:16 and SEQ ID NO:12;

d) SEQ ID NO:16 and SEQ ID NO:18;

e) SEQ ID NO:17 and SEQ ID NO:12;

f) SEQ ID NO:1 and SEQ ID NO:27;

g) SEQ ID NO:24 and SEQ ID NO:25; and

h) SEQ ID NO:21 and SEQ ID NO:4.

4. A pair of oligonucleotide primers, wherein said pair consists of SEQ ID NO:16 and SEQ ID NO:12.

5. A pair of oligonucleotide primers, wherein said pair consists of SEQ ID NO:16 and SEQ ID NO:18.

6. A pair of oligonucleotide primers, wherein said pair consists of SEQ ID NO:17 and SEQ ID NO:12.

7. A pair of oligonucleotide primers, wherein said pair consists of SEQ ID NO:24 and SEQ ID NO:25.

8. A method for the detection of a fungal pathogen, comprising the steps of:

(a) isolating DNA from a plant tissue infected with a pathogen;

(b) subjecting said DNA to polymerase chain reaction amplification using at least one primer according to claim 1; and

(c) detecting said fungal pathogen by visualizing the product or products of said polymerase chain reaction amplification.

9. The method of claim 8, wherein said fungal pathogen is *Colletotrichum acutatum, Alternaria* spp., and *Cladosporium carpophilum.*

10. A method for the detection of a fungal pathogen, comprising the steps of:

(a) isolating DNA from a plant tissue infected with said fungal pathogen;

(b) amplifying a part of the Internal Transcribed Spacer sequence of said fungal pathogen using said DNA as a template in a polymerase chain reaction with a pair of primers according to claim 2; and

(c) detecting sad fungal pathogen by visualizing the amplified part of the Internal Transcribed Spacer sequence.

11. The method of claim 10, wherein said fungal pathogen is *Colletotrichum acutatum, Alternaria* spp., and *Cladosporium carpophilum.*

12. The method of claim 10, wherein said pair of primers is according to claim 3.

13. The method of claim 10, wherein said pair of primers is according to claim 4.

14. The method of claim 10, wherein said pair of primers is according to claim 5.

15. The method of claim 10, wherein said pair of primers is according to claim 6.

16. The method of claim 10, wherein said pair of primers is according to claim 7.

19. A diagnostic kit used in detecting a fungal pathogen, comprising the primer of claim 1.

20. A diagnostic kit used in detecting a fungal pathogen, comprising the pair of primers of claim 2.

21. A diagnostic kit used in detecting a fungal pathogen, comprising the pair of primers of claim 3.

22. A diagnostic kit used in detecting a fungal pathogen, comprising the pair of primers of claim 4.

23. A diagnostic kit used in detecting a fungal pathogen, comprising the pair of primers of claim 5.

24. A diagnostic kit used in detecting a fungal pathogen, comprising the pair of primers of claim 6.

25. A diagnostic kit used in detecting a fungal pathogen, comprising the pair of primers of claim 7.

26. A DNA extraction buffer, comprising:
(a) approximately 100 mM Tris, pH 8.0;
(b) 0.2-2.0 M NaCl;
(c) 1-200 mM ethylenediaminetetraacetic acid (EDTA);
(d) 0.1-5% w/v hexadecyltrimethylammonium (CTAB);
(e) 0.1-5% w/v polyvinylpyrolidine (PVP); and
(f) 0.01-2% w/v ascorbic acid.

27. The DNA extraction buffer of claim 26, comprising: 100 mM Tris, pH 8.0; 1.4 M NaCl; 20 mM EDTA; 2% w/v CTAB; 2% w/v PVP and 0.1% w/v ascorbic acid.

28. The DNA extraction buffer of claim 26, comprising 100 mM Tris, pH 8.0.

29. The DNA extraction buffer of claim 26, comprising 1.4 M NaCl.

30. The DNA extraction buffer of claim 26, comprising 20 mM EDTA.

31. The DNA extraction buffer of claim 26, comprising 2% w/v CTAB.

32. The DNA extraction buffer of claim 26, comprising 2% w/v PVP.

33. The DNA extraction buffer of claim 26, comprising 0.1% w/v ascorbic acid.

34. A method for preparing an extract of DNA from tissue, comprising the steps of:
(a) taking a plurality of random tissue samples from an organism population;
(b) adding the extraction buffer of claim 26, to the tissue samples;
(c) macerating the tissue samples and extraction buffer to form an extract; and
(d) removing the extract from the macerated tissue and buffer.

35. The method of claim 34, wherein the organism population is a plant population.

36. The method of claim 35, wherein the tissue samples are selected from leaves, stems, roots, blossoms, immature flowers, peduncles, hulls, fruits, immature fruits, or woody tissue.

37. The method of claim 34, wherein the extraction buffer comprises: 100 mM Tris, pH 8.0; 1.4 M NaCl; 20 mM EDTA; 2% w/v CTAB; 2% w/v PVP and 0.1% w/v ascorbic acid.

38. A method for performing PCR analysis on DNA extracted from tissue, comprising the steps of:
(a) taking a plurality of random tissue samples from an organism population;
(b) adding the extraction buffer of claim 26, to the tissue samples;
(c) macerating the tissue samples and extraction buffer to form an extract;
(d) removing the extract from the macerated tissue and buffer; and
(e) performing PCR analysis on the extract.

39. The method of claim 38, further comprising the step of boiling the extract after removing it from the macerated tissue and buffer.

40. The method of claim 39, further comprising the step of diluting the extract.

41. The method of claim 40, wherein the organism population is a plant population.

42. The method of claim 41, wherein the tissue samples are selected from leaves, stems, roots, blossoms, immature flowers, peduncles, hulls, fruits, immature fruits, or woody tissue.

43. The method of claim 38, wherein the extraction buffer comprises: 100 mM Tris, pH 8.0; 1.4 M NaCl; 20 mM EDTA; 2% w/v CTAB; 2% w/v PVP and 0.1% w/v ascorbic acid.

44. The method of claim 41, wherein the plant tissue is from a stone fruit plant population.

5

45. The method of claim 8, wherein the plant tissue is from a stone fruit plant.

46. The method of claim 8, wherein the plant tissue is from an almond plant.